

SEQUENCE LISTING

<110> YAMAMOTO, Kazuo  
Sumitomo Corporation

<120> Carbohydrate library constructed by Gene Alteration of Cargo  
Receptors

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<150> JP 2002-238559

<151> 2002-08-19

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<170> PatentIn Ver. 2.0

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<221> CDS

<222> (22)..(1554)

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gcc	aga	gtt	cgg	ccg	ctg	ttc	tgc	gcc	ttg	ctg	ctg	tca	ctc	ggt	cgc	99
Ala	Arg	Val	Arg	Pro	Leu	Phe	Cys	Ala	Leu	Leu	Leu	Ser	Leu	Gly	Arg	
				15					20					25		

ttc	gtc	cgg	ggc	gac	ggc	gtg	gga	gga	gac	ccc	gcg	gtc	gcg	ttg	cca	147
Phe	Val	Arg	Gly	Asp	Gly	Val	Gly	Gly	Asp	Pro	Ala	Val	Ala	Leu	Pro	

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cat	cgc	cgt	ttc	gag	tac	aaa	tac	agc	ttc	aag	ggg	ccg	cac	ctg	gtg	195														
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Gln	Ser	Asp	Gly	Thr	Val	Pro	Phe	Trp	Ala	His	Ala	Gly	Asn	Ala	Ile															
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Pro	Ser	Ser	Asp	Gln	Ile	Arg	Val	Ala	Pro	Ser	Leu	Lys	Ser	Gln	Arg															
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Glu	Val	Thr	Phe	Arg	Val	Thr	Gly	Arg	Gly	Arg	Ile	Gly	Ala	Asp	Gly															
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 Asn Met Ile Ile Pro Ala Gln Gly His Phe Gly Ile Ser Ala Ala Thr  
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 Leu Thr Glu Pro Gly Lys Glu Pro Pro Thr Pro Asp Lys Glu Ile Ser  
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 Glu Leu Asp Lys Lys Lys Glu Glu Phe Gln Lys Gly His Pro Asp Leu  
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 Gln Gly Gln Pro Ala Glu Glu Ile Phe Glu Ser Val Gly Asp Arg Glu  
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 Val Ser Ser Leu Thr Glu Glu Ile Ser Lys Arg Gly Ala Gly Met Pro  
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 Lys Lys Phe Phe  
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<213> Homo sapiens

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Val	Gly	Gly	Asp	Pro	Ala	Val	Ala	Leu	Pro	His	Arg	Arg	Phe	Glu	Tyr
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Lys	Tyr	Ser	Phe	Lys	Gly	Pro	His	Leu	Val	Gln	Ser	Asp	Gly	Thr	Val
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Pro	Phe	Trp	Ala	His	Ala	Gly	Asn	Ala	Ile	Pro	Ser	Ser	Asp	Gln	Ile	65	70	75	80
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Glu	Asn	Gln	Gly	Leu	Glu	Gly	Pro	Val	Phe	Gly	Ser	Ala	Asp	Leu	Trp	130	135	140	
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Asp	His	Gln	Asn	Asp	Gly	Ala	Ser	Gln	Ala	Leu	Ala	Ser	Cys	Gln	Arg	180	185	190	
Asp	Phe	Arg	Asn	Lys	Pro	Tyr	Pro	Val	Arg	Ala	Lys	Ile	Thr	Tyr	Tyr	195	200	205	
Gln	Asn	Thr	Leu	Thr	Val	Met	Ile	Asn	Asn	Gly	Phe	Thr	Pro	Asp	Lys	210	215	220	
Asn	Asp	Tyr	Glu	Phe	Cys	Ala	Lys	Val	Glu	Asn	Met	Ile	Ile	Pro	Ala	225	230	235	240
Gln	Gly	His	Phe	Gly	Ile	Ser	Ala	Ala	Thr	Gly	Gly	Leu	Ala	Asp	Asp	245	250	255	
His	Asp	Val	Leu	Ser	Phe	Leu	Thr	Phe	Gln	Leu	Thr	Glu	Pro	Gly	Lys	260	265	270	
Glu	Pro	Pro	Thr	Pro	Asp	Lys	Glu	Ile	Ser	Glu	Lys	Glu	Lys	Glu	Lys	275	280	285	
Tyr	Gln	Glu	Glu	Phe	Glu	His	Phe	Gln	Gln	Glu	Leu	Asp	Lys	Lys	Lys	290	295	300	

Glu Glu Phe Gln Lys Gly His Pro Asp Leu Gln Gly Gln Pro Ala Glu  
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Glu Ile Phe Glu Ser Val Gly Asp Arg Glu Leu Arg Gln Val Phe Glu  
325 330 335

Gly Gln Asn Arg Ile His Leu Glu Ile Lys Gln Leu Asn Arg Gln Leu  
340 345 350

Asp Met Ile Leu Asp Glu Gln Arg Arg Tyr Val Ser Ser Leu Thr Glu  
355 360 365

Glu Ile Ser Lys Arg Gly Ala Gly Met Pro Gly Gln His Gly Gln Ile  
370 375 380

Thr Gln Gln Glu Leu Asp Thr Val Val Lys Thr Gln His Glu Ile Leu  
385 390 395 400

Arg Gln Val Asn Glu Met Lys Asn Ser Met Ser Glu Thr Val Arg Leu  
405 410 415

Val Ser Gly Met Gln His Pro Gly Ser Ala Gly Gly Val Tyr Glu Thr  
420 425 430

Thr Gln His Phe Ile Asp Ile Lys Glu His Leu His Ile Val Lys Arg  
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Asp Ile Asp Asn Leu Val Gln Arg Asn Met Pro Ser Asn Glu Lys Pro  
450 455 460

Lys Cys Pro Glu Leu Pro Pro Phe Pro Ser Cys Leu Ser Thr Val His  
465 470 475 480

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Leu Gly Arg Pro Gly Leu Leu Gly Pro Gly Pro Gly Pro Thr Thr Pro	
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ctc ttt ctt ctt ttg ttg ttg ggg tct gtg act gcg gat ata act gac	144
Leu Phe Leu Leu Leu Leu Leu Gly Ser Val Thr Ala Asp Ile Thr Asp	
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ggc aac agt gaa cat ctc aag cgg gag cat tcg ctc att aag ccc tac	192
Gly Asn Ser Glu His Leu Lys Arg Glu His Ser Leu Ile Lys Pro Tyr	
50 55 60	
caa ggg gtc ggt tcc agc tct atg ccc ctc tgg gac ttc cag ggc agc	240
Gln Gly Val Gly Ser Ser Ser Met Pro Leu Trp Asp Phe Gln Gly Ser	
65 70 75 80	
act atg ctc acg agc cag tac gta cgt ctg acc cct gac gag cgc agc	288
Thr Met Leu Thr Ser Gln Tyr Val Arg Leu Thr Pro Asp Glu Arg Ser	
85 90 95	
aaa gag ggc tct atc tgg aac cac cag ccg tgc ttc ctc aaa gac tgg	336
Lys Glu Gly Ser Ile Trp Asn His Gln Pro Cys Phe Leu Lys Asp Trp	
100 105 110	
gaa atg cac gtc cac ttc aaa gtc cac ggc aca ggg aag aag aac ctc	384
Glu Met His Val His Phe Lys Val His Gly Thr Gly Lys Lys Asn Leu	
115 120 125	
cat gga gac ggc atc gcc ttg tgg tac acc cgg gac cgc ctc gtg cca	432
His Gly Asp Gly Ile Ala Leu Trp Tyr Thr Arg Asp Arg Leu Val Pro	
130 135 140	
ggg cct gtg ttt gga agc aaa gat aac ttc cac ggc tta gcc atc ttc	480



Gly	Pro	Val	Phe	Gly	Ser	Lys	Asp	Asn	Phe	His	Gly	Leu	Ala	Ile	Phe	
145					150					155					160	
ctg	gac	acc	tac	ccc	aat	gat	gag	acc	act	gag	cgc	gtg	ttc	ccg	tac	528
Leu	Asp	Thr	Tyr	Pro	Asn	Asp	Glu	Thr	Thr	Glu	Arg	Val	Phe	Pro	Tyr	
				165					170				175			
atc	tcg	gtg	atg	gtg	aac	aat	ggc	tcc	ctg	tcc	tac	gac	cac	agc	aag	576
Ile	Ser	Val	Met	Val	Asn	Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Ser	Lys	
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Asp	Gly	Arg	Trp	Thr	Glu	Leu	Ala	Gly	Cys	Thr	Ala	Asp	Phe	Arg	Asn	
		195					200					205				
cgc	gat	cac	gac	acc	ttc	ctg	gct	gtg	cgc	tac	tcc	cgg	ggc	cgt	ctg	672
Arg	Asp	His	Asp	Thr	Phe	Leu	Ala	Val	Arg	Tyr	Ser	Arg	Gly	Arg	Leu	
	210					215					220					
acg	gtg	atg	acc	gac	ctg	gag	gac	aag	aac	gag	tgg	aag	aac	tgc	att	720
Thr	Val	Met	Thr	Asp	Leu	Glu	Asp	Lys	Asn	Glu	Trp	Lys	Asn	Cys	Ile	
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gac	atc	acg	gga	gtg	cgc	ctg	ccc	acc	ggc	tac	tac	ttc	ggg	gcc	tcc	768
Asp	Ile	Thr	Gly	Val	Arg	Leu	Pro	Thr	Gly	Tyr	Tyr	Phe	Gly	Ala	Ser	
			245					250					255			
gcc	ggc	acc	ggc	gac	ctg	tct	gac	aat	cat	gac	atc	atc	tcc	atg	aag	816
Ala	Gly	Thr	Gly	Asp	Leu	Ser	Asp	Asn	His	Asp	Ile	Ile	Ser	Met	Lys	
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ctg	ttc	cag	ctg	atg	gtg	gag	cac	acg	ccc	gac	gag	gag	agc	atc	gac	864
Leu	Phe	Gln	Leu	Met	Val	Glu	His	Thr	Pro	Asp	Glu	Glu	Ser	Ile	Asp	
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tgg	acc	aag	atc	gag	ccc	agc	gtc	aac	ttc	ctc	aag	tcg	ccc	aaa	gac	912
Trp	Thr	Lys	Ile	Glu	Pro	Ser	Val	Asn	Phe	Leu	Lys	Ser	Pro	Lys	Asp	
	290					295				300						
aac	gtg	gac	gac	ccc	acg	ggg	aac	ttc	cgc	agc	ggg	ccc	ctg	acg	ggg	960
Asn	Val	Asp	Asp	Pro	Thr	Gly	Asn	Phe	Arg	Ser	Gly	Pro	Leu	Thr	Gly	
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tgg	cgg	gtg	ttc	ctg	ctg	ctg	ctg	tgc	gct	ctc	ctg	ggc	atc	gtt	gtc	1008
Trp	Arg	Val	Phe	Leu	Leu	Leu	Leu	Cys	Ala	Leu	Leu	Gly	Ile	Val	Val	

325

330

335

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 Cys Ala Val Val Gly Ala Val Val Phe Gln Lys Arg Gln Glu Arg Asn  
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 Lys Arg Phe Tyr  
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<212> PRT

<213> Homo sapiens

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Leu Phe Leu Leu Leu Leu Leu Gly Ser Val Thr Ala Asp Ile Thr Asp  
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Gly Asn Ser Glu His Leu Lys Arg Glu His Ser Leu Ile Lys Pro Tyr  
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Gln Gly Val Gly Ser Ser Ser Met Pro Leu Trp Asp Phe Gln Gly Ser  
       65                  70                  75                  80

Thr Met Leu Thr Ser Gln Tyr Val Arg Leu Thr Pro Asp Glu Arg Ser  
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Lys Glu Gly Ser Ile Trp Asn His Gln Pro Cys Phe Leu Lys Asp Trp

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His Gly Asp Gly Ile Ala Leu Trp Tyr Thr Arg Asp Arg Leu Val Pro		
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Gly Pro Val Phe Gly Ser Lys Asp Asn Phe His Gly Leu Ala Ile Phe		
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Leu Asp Thr Tyr Pro Asn Asp Glu Thr Thr Glu Arg Val Phe Pro Tyr		
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Ile Ser Val Met Val Asn Asn Gly Ser Leu Ser Tyr Asp His Ser Lys		
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Asp Gly Arg Trp Thr Glu Leu Ala Gly Cys Thr Ala Asp Phe Arg Asn		
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Arg Asp His Asp Thr Phe Leu Ala Val Arg Tyr Ser Arg Gly Arg Leu		
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Thr Val Met Thr Asp Leu Glu Asp Lys Asn Glu Trp Lys Asn Cys Ile		
225	230	235
Asp Ile Thr Gly Val Arg Leu Pro Thr Gly Tyr Tyr Phe Gly Ala Ser		
245	250	255
Ala Gly Thr Gly Asp Leu Ser Asp Asn His Asp Ile Ile Ser Met Lys		
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Leu Phe Gln Leu Met Val Glu His Thr Pro Asp Glu Glu Ser Ile Asp		
275	280	285
Trp Thr Lys Ile Glu Pro Ser Val Asn Phe Leu Lys Ser Pro Lys Asp		
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Asn Val Asp Asp Pro Thr Gly Asn Phe Arg Ser Gly Pro Leu Thr Gly		
305	310	315
Trp Arg Val Phe Leu Leu Leu Cys Ala Leu Leu Gly Ile Val Val		
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Cys Ala Val Val Gly Ala Val Val Phe Gln Lys Arg Gln Glu Arg Asn		

340

345

350

Lys Arg Phe Tyr  
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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: synthetic  
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29

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&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: synthetic  
oligonucleotide

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&lt;211&gt; 53

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: synthetic  
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&lt;220&gt;

&lt;223&gt; N=A, T, C or G

&lt;400&gt; 7

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<223> Description of Artificial Sequence: synthetic  
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30

<210> 9  
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<223> Description of Artificial Sequence: synthetic  
oligonucleotide

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24

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oligonucleotide

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24

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16

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<400> 12

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23

<210> 13

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic  
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30

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<220>

<223> N=A, T, C or G

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32

<210> 16

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic  
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<400> 16

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27

<210> 17

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Asp Pro Asp Ser Asn Gly Gly Ser Phe

1

5